IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C7
Serial No:	10/006,130	Group Art Unit:	1647
Filed:	December 6, 2001	Examiner:	Rachel B. Kapust

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
Washington, D.C. 20231

DECLARATION OF AUDREY GODDARD, Ph.D. UNDER 37 CFR 1.131

I, Audrey Goddard, Ph.D. do hereby declare and say as follows:

1. I am Senior Clinical Scientist at the Diagnostics, Development Sciences Department of Genentech, Inc., South San Francisco, CA 94080.

2. I am one of the inventors of the above-identified application.

3. I have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

4. I, along with other inventors of this application, conceived and reduced to practice the polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States prior to August 14, 1998.

5. At the time the PRO1244 polypeptide was cloned and sequenced I was responsible for overseeing the sequencing of novel polypeptides, including the PRO1244 polypeptide (SEQ ID NO:130) claimed in the above-identified application.

6. A cDNA clone, referred to as DNA64883-1526 in the above-identified application, was identified as encoding the PRO1244 polypeptide.

7. The full length of the cDNA clone is shown in Figure 73 of the above-identified application. The full-length cDNA sequence has 2213 nucleotide residues. The full length of the PRO1244 peptide encoded by DNA64883-1526 is shown in Figure 74 of

the above-identified application. The full-length PRO1244 polypeptide has 335 amino acid residues.

8. Copies of the pages from the GSeqEdit database which report the cloning and sequencing data for the PRO1244 polypeptide sequence and its encoding nucleic acid sequence are attached to this declaration (with the dates redacted) as Exhibit A.

9. The GSeqEdit report shows the full-length nucleic acid sequence for DNA-64883-1526 (identified as "DNA-64883") and the full-length PRO1244 polypeptide encoded by DNA 64883. Both the DNA-64883 and the PRO1244 polypeptide sequences were obtained prior to August 14, 1998.

10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

11. The beginning of the cDNA sequence corresponding to SEQ ID NO: 129 in the above-identified application is shown on page 1 of the GSeqEdit database report and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The location of the last nucleotide corresponding to SEQ ID NO: 129 is shown on page 11 and is marked with an arrow.

12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. Exhibit A clearly shows that both the full-length DNA-64883 sequence and the full-length PRO1244 polypeptide sequence disclosed in the above-identified application were obtained prior to August 14, 1998.

15. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001

of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard

6/14/04
Date

SV 2037583 v1
6/15/04 3:02 PM (39780.2830)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C7
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For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
Washington, D.C. 20231

DECLARATION OF WILLIAM WOOD, Ph.D. UNDER 37 CFR 1.131

I, William Wood, Ph.D. do hereby declare and say as follows:

1. I am Director and Staff Scientist at the Department of Bioinformatics, of Genentech, Inc., South San Francisco, CA 94080.

2. I am one of the inventors of the above-identified application.

3. I have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

4. I, along with other inventors of this application, conceived and reduced to practice the polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States prior to August 14, 1998.

5. At the time the PRO1244 polypeptide was cloned and sequenced I was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA that encoded PRO1244 polypeptide (SEQ ID NO:130) claimed in the above-identified application.

6. A cDNA clone, referred to as DNA64883-1526 in the above-identified application, was identified as encoding the PRO1244 polypeptide.

7. The full length of the cDNA clone is shown in Figure 73 of the above-identified application. The full-length cDNA sequence has 2213 nucleotide residues. The full

length of the PRO1244 peptide encoded by DNA64883-1526 is shown in Figure 74 of the above-identified application. The full-length PRO1244 polypeptide has 335 amino acid residues.

8. Copies of the pages from the GSeqEdit database which report the cloning and sequencing data for the PRO1244 polypeptide sequence and its encoding nucleic acid sequence are attached to this declaration (with the dates redacted) as Exhibit A.

9. The GSeqEdit report shows the full-length nucleic acid sequence for DNA-64883-1526 (identified as "DNA-64883") and the full-length PRO1244 polypeptide encoded by DNA 64883. Both the DNA-64883 and the PRO1244 polypeptide sequences were obtained prior to August 14, 1998.

10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

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12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. Exhibit A clearly shows that both the full-length DNA-64883 sequence and the full-length PRO1244 polypeptide sequence disclosed in the above-identified application were obtained prior to August 14, 1998.

15. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and

the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

William Wood

6/14/04
Date

SV 2037583 v1
6/9/04 1:21 PM (39780.2830)

Exhibit A
to Declarations of Audrey Goddard and William Wood under 37 CFR 1.131

GSeqEdit Database Report

>[redacted]
>DNA64883 [Full]
>510 Sites [All Sites]
>[redacted] DNA64883 wiw GSeqEdit
>[redacted] DNA64883 zemin GSeqEdit
>[redacted] DNA64883 goddarda GSeqEdit
>[redacted] DNA64883 sheldens GSeqEdit
>HBN64883.seq, sequenced at ABI/ACGT by Peter Ma and Ellson Chen
>human ortholog of implantation-associated protein - Rattus

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                                                                  nlaIII
             mnlI                                                 mslI
            taqI                                                 styI
           xhoI                 thaI                             ncoI
           tliI                 fnuDII/mvnI                      dsaI        tseI
           smlI                hinPI    aciI                     btgI/bstDSI fnu4HI/bsoFI
           paeR7I  mwoI     tseI bstUI[M.hhaI-]                  bstXI       bbvI                  dde
      tsp509I[M.ecoRI-]     fnu4HI/bsoFI                         bsaJI     hinPI               taiI   bsp
     ecoRI    avaI[M.taqI-] bbvI bsh1236I                    tsp45I        hhaI/cfoI           maeII/hpyC
     apoI   mwoI bseRI   nlaIII hhaI/cfoI               bsmAI maeIII      haeII             hpy99I   mnlI
1 CGGAATTCGG CTCGAGGAGC GAACATGGCA GCGCGTTGGC GGTTTTGGTG TGTCTCTGTG ACCATGGTGG TGGCGCTGCT CATCGTTTGC GACGTTCCCT
  GCCTTAAGCC GAGCTCCTCG CTTGTACCGT CGCGCAACCG CCAAAACCAC ACAGAGACAC TGGTACCACC ACCGCGACGA GTAGCAAACG CTGCAAGGGA
1                          M  A  A  R  W  R  F  W  C  V  S  V  T  M  V  V  A  L  L  I  V  C  D  V  P  S
                 ^insert starts here
                           ^MET
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      mnlI                                                             aluI
    alwNI[dcm-]                                                        pvuII
    alw26I/bsmAI          bsaXI          hpy188I           mspA1I/nspBII                                                       bsmAI
101 CAGCCTCTGC CCAAAGAAAG AAGGAGATGG TGTTATCTGA AAAGGTTAGT CAGCTGATGG AATGGACTAA CAAAAGACCT GTAATAAGAA TGAATGGAGA
    GTCGGAGACG GGTTTCTTTC TTCCTCTACC ACAATAGACT TTTCCAATCA GTCGACTACC TTACCTGATT GTTTTCTGGA CATTATTCTT ACTTACCTCT
27   A  S  A   Q  R  K   K  E  M  V   L  S  E   K  V  S   Q  L  M  E   W  T  N   K  R  P   V  I  R  M   N  G  D

                                                                 tspRI                    bst4CI/hpyCH4III    cac8I
                                                                 btsI                    ahdI/eam1105I     cac8I
         hpy99I                          tsp509I           nlaIII                    hpyCH4V tspRI         hpyCH4V al
201 CAAGTTCCGT CGCCTTGTGA AAGCCCCACC GAGAAATTAC TCCGTTATCG TCATGTTCAC TGCTCTCCAA CTGCATAGAC AGTGTGTCGT TTGCAAGCAA
    GTTCAAGGCA GCGGAACACT TTCGGGGTGG CTCTTTAATG AGGCAATAGC AGTACAAGTG ACGAGAGGTT GACGTATCTG TCACACAGCA AACGTTCGTT
60   K  F  R   R  L  V  K   A  P  P   R  N  Y   S  V  I  V   M  F  T   A  L  Q   L  H  R  Q   C  V  V   C  K  Q
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                                  scrFI[dcm-]
                                  pspGI
                                  mvaI
                                  ecoRII[dcm-]
                                  dsaV[dcm-]
                                  bstNI
                                  bssKI[dcm-]
                                  apyI[dcm+]
                               sau3AI
                               mboI/ndeII[dam-]
                               dpnII[dam-]
                               dpnI[dam+]
                               alwI[dam-]        scrFI[dcm-]
                              bstYI/xhoII        pspGI
                             alwNI[dcm-]         mvaI                                    nlaIII
                             alw26I/bsmAI        ecoRII[dcm-]                            styI
                          tsp509I[M.ecoRI-]      dsaV[dcm-]       hpyCH4V                ncoI
                       ecoRI pflMI[dcm-]         bstNI baeI    tspRI                     dsaI
                       apoI  bslI[dcm-]          bssKI[dcm-]  bsrI bsmI hphI             btgI/bstDSI
                    mboII   hpy188III            apyI[dcm+] bpmI/gsuI[dcm-]              bsaJI                    hpy18
301 GCTGATGAAG AATTCCAGAT CCTGGCAAAC TCCTGGCGAT ACTCCAGTGC ATTCACCAAC AGGATATTTT TTGCCATGGT GGATTTTGAT GAAGGCTCTG
    CGACTACTTC TTAAGGTCTA GGACCGTTTG AGGACCGCTA TGAGGTCACG TAAGTGGTTG TCCTATAAAA AACGGTACCA CCTAAAACTA CTTCCGAGAC
 93 A  D  E  E  F  Q  I  L  A  N  S  W  R  Y  S  S  A  F  T  N  R  I  F  F  A  M  V  D  F  D  E  G  S  D
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```
                      tsp509I[M.ecoRI-]
                     ecoRI                                hpyCH4V
            sfaNI    apoI                                ecoNI
         hpy188I   nlaIII    aluI                        bslI         bslI       hphI      ndeI     maeIII      aciI
401 ATGTATTTCA GATGCTAAAC ATGAATTCAG CTCCAACTTT CATCAACTTT CCTGCAAAAG GGAAACCCAA ACGGGGTGAT ACATATGAGT TACAGGTGCG
    TACATAAAGT CTACGATTTG TACTTAAGTC GAGGTTGAAA GTAGTTGAAA GGACGTTTTC CCTTTGGGTT TGCCCCACTA TGTATACTCA ATGTCCACGC
127   V  F  Q   M  L  N   M  N  S  A   P  T  F   I  N  F   P  A  K  G   K  P  K   R  G  D   T  Y  E  L   Q  V  R

            ddeI[M.aluI-]
            bspCNI        mspI    sau3AI
           celII/espI     hpaII   mboI/ndeII[dam-]
           blpI/bpu1102I scrFI[M.hpaII-]                                                          bsmFI
          aluI            nciI    dpnII[dam-]                                                     sau96I
         pvuII            dsaV    dpnI[dam+]                                                      nlaIV
         mspAII/nspBII    bssKI alwI[dam-]                 sspI                       tsp509I    avaII bslI
501 GGGTTTTTCA GCTGAGCAGA TTGCCCGGTG GATCGCCGAC AGAACTGATG TCAATATTAG AGTGATTAGA CCCCCAAATT ATGCTGGTCC CCTTATGTTG
    CCCAAAAAGT CGACTCGTCT AACGGGCCAC CTAGCGGCTG TCTTGACTAC AGTTATAATC TCACTAATCT GGGGGTTTAA TACGACCAGG GGAATACAAC
160 G  F  S   A  E  Q  I   A  R  W   I  A  D   R  T  D  V   N  I  R   V  I  R   P  P  N  Y   A  G  P   L  M  L

                                 taqI                                                                aluI
                                sfuI                                                                tseI
                                bstBI                                           fokI               fnu4HI/bsoFI
                                bsiCI                     tsp509I    tru9I      bstF5I             bbvI
                          baeI  mboII mboII              apoI       mseI      bsrI      mwoI hpyCH4V
601 GGATTGCTTT TGGCTGTTAT TGGTGGACTT GTGTATCTTC GAAGAAGTAA TATGGAATTT CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT
    CCTAACGAAA ACCGACAATA ACCACCTGAA CACATAGAAG CTTCTTCATT ATACCTTAAA GAGAAATTAT TTTGACCTAC CCGAAAACGT CGAAACACAA
193 G  L  L  L   A  V  I   G  G  L   V  Y  L  R   R  S  N   M  E  F   L  F  N  K   T  G  W   A  F  A   A  L  C  F
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                                                                                               nlaIII          nlaIII
                                                                                              pciI            styI
                                                                                              nspHI           ncoI
                                         sau96I                           bslI                nspI            dsaI
                                         avaII                        tfiI                    aflIII          btgI/bs
        cac8I      ahdI/eam1105I    nlaIV    mnlI       ndeI          hinfI         bsmFI          tsp509I    bsaJI
701 TTGTGCTTGC TATGACATCT GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA CATGTGAATT ATATCCATGG
    AACACGAACG ATACTGTAGA CCAGTTTACA CCTTGGTATA TTCTCCTGGT GGTATACGGG TATTCTTAGG GGTGTGCCCT GTACACTTAA TATAGGTACC
227   V  L  A   M  T  S   G  Q  M  W   N  H  I   R  G  P   P  Y  A  H   K  N  P   H  T  G   H  V  N  Y   I  H  G

                                                                      ddeI                            tseI
                                                                      eco81I                          fnu4HI/bsoFI
                                                     tru9I            bsu36I/mstII/sauI               bbvI        hpy1
             bsrI       aluI              mboII      mseI        maeIII                              aluI       mnlI
801 AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT
    TTCGTCAGTT CGGGTCAAAC ATCGACTTTG TGTGTAACAA GAAGACAAAT TACCACCTCA ATGGAATCCT TACCACGAAA ATACACTTCG ACGATGGAGA
260  S  S  Q   A  Q  F  V   A  E  T   H  I  V   L  L  F  N   G  G  V   T  L  G   M  V  L  L   C  E  A   A  T  S

                                                                                                      sau3AI
                                                                                                      mboI/ndeII[dam
                                                                                                      dpnII[dam-]
                                                                                 sfaNI                dpnI[dam+]
                                                                       eco57I   fokI                 bstYI/xhoII
      nlaIII                                                           mboII    bstF5I               bglII        nl
901 GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC
    CTGTACCTAT AACCTTTCGC TTTCTATTAC ACACACCGAC CATAACCTGA ACAACATAAT AAGAAGTCAA CCTACGAGAG ATAAAAATCT AGATTTATAG
293 D  M  D  I   G  K  R   K  I  M   C  V  A  G   I  G  L   V  V  L   F  F  S  W   M  L  S   I  F  R   S  K  Y  H
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                                                   bsmFI
                                                   sau96I                          bsrI
                                                   nlaIV                         rsaI
                                                   avaII                  bpmI/gsuI[dcm-]
                                            tru9I  ppuMI                  bsrI   csp6I
                              aluI hpy188I  mseI   eco0109I/draII         tspRI  scaI     tsp509I
1001 ATGGCTACCC ATACAGCTTT CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC GAAAATCGTG TGTGTTTGAA
     TACCGATGGG TATGTCGAAA GACTACTCAA TTTTTCCAGG GTCTCTATAT ATCTGTGACC TCATGACCTT TAACTTTTTG CTTTTAGCAC ACACAAACTT
327   G  Y  P   Y  S  F   L  M  S  O

                                                             tru9I
                                                             mseI    tru9I
        bsmI                                               ahaIII/draI     tru9I                      tru9I
     mboII hpyCH4V                          mnlI           swaI      mseI  mseI     mboII              mseI
1101 AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC
     TTCTTCTTAC GTTGAACATA TAAAACATAA TGGAGAAAAA AAGTTCACTA AATTTATCAA TTAGTAAATT GGTTTCTTCT ACACATCACG GAATTGTTCG

                                mnlI
                              ddeI                                  bsrI                   tsp509I      tru9I
                              bspCNI                 mnlI tru9I   mboII tspRI            tru9I    rsaI tsp509I
       mnlI                   hpy188I           tsp509I    mseI   earI/ksp632I           mseI     csp6I  mseI
1201 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT
     TTAGGAGACA GTTTTAGACT CCATAAACTT TTATTAATAG GAGAATTGGA AGAGAAGGGT CACTTGAAAT ACCTTGTAAA TTAAATCATG TTAATTCATA

                                                                          tru9I
                                                                          mseI
                                                                         hpaI
       psiI    tsp509I                                   aluI            hincII/hindII hpy188I              bslI
1301 ATTATAAAAA TTGTAAAACT ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT TTTATATTGC CTTATCCAAA
     TAATATTTTT AACATTTTGA TGATGAAACA AAATCAATCT TGTTTCGAGT TTTGATGAAA TCAATTGAAC CAGTAGACTA AAATATAACG GAATAGGTTT
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                          scrFI[dcm-]
                          pspGI
                          mvaI
                          ecoRII[dcm-]
                          dsaV[dcm-]
                          bstNI                                    tsp509I[M.ecoRI-]
                          bssKI[dcm-]                             xmnI
                          apyI[dcm+]                              ecoRI          mboII
                         sexAI                                    asp700      aluI     mslI        fokI
                    hpy188III          ndeI     maeIII           apoI      ddeI[M.aluI-]          bstF5I
1401 GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT
     CTACCCCTTT CATTCAGGAC TGGTCCACAA GGGTGTATAC GGACAATGTC TATTGATGTA ATCCTTAAGT AAGAATCGAA GAAGTAGAAA CACACCTACA

                                                                                          taiI
                                                                                      hgiAI/aspHI
                                                                                      bsp1286
                                                          hpy188I                     bsiHKAI    rmaI  ddeI
     bstZ17I                                             mboII                    hpy188I   maeII/hpyCH4IV
     bst1107I                                           bpuAI                    eco57I    aflIII maeI  bspC
     accI       sfaNI                    tsp509I     nlaIII bbsI                mboII  bmyI btrI  bfaI mnlI
1501 GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC
     CATATGAAAT GCGTAGAAAG GAAAACTCAT CTCTTTAATA CACACAGTAC ACCAGAAGAC TTTTACCTTG TGGTAAGAAG TCTCGTGTGC AGATCGGGAG
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                                                                                 tth111I/aspI
                                                                                 pleI
                 bseRI                                                           pflFI
                mnlI                                  bpmI/gsuI[dcm-]            mlyI
               bseRI                               hinPI      ddeI               hinfI
          bst4CI/hpyCH4III mnlI  hpyCH4V           hhaI/cfoI  bspCNI           bsmAI     bsmAI
1601 AGCAAGACAG TTGTTTCTCC TCCTCCTTGC ATATTTCCTA CTGCGCTCCA GCCTGAGTGA TAGAGTGAGA CTCTGTCTCA AAAAAAAGTA TCTCTAAATA
     TCGTTCTGTC AACAAAGAGG AGGAGGAACG TATAAAGGAT GACGCGAGGT CGGACTCACT ATCTCACTCT GAGACAGAGT TTTTTTTCAT AGAGATTTAT

                                tru9I                                                                 tsp45I
                                mseI                         tfiI                                    hphI
          tsp509I              hpaI                xmnI      hinfI                              tru9I maeIII
        psiI         smlI      hincII/hindII       asp700  hpy188I                ddeI          mseI bstEII
1701 CAGGATTATA ATTTCTGCTT GAGTATGGTG TTAACTACCT TGTATTTAGA AAGATTTCAG ATTCATTCCA TCTCCTTAGT TTTCTTTTAA GGTGACCCAT
     GTCCTAATAT TAAAGACGAA CTCATACCAC AATTGATGGA ACATAAATCT TTCTAAAGTC TAAGTAAGGT AGAGGAATCA AAAGAAAATT CCACTGGGTA

                                                                                                        dde
                 ddeI[M.aluI-]     maeIII         haeIII/palI                     tsp45I             rsaI
                aluI             tspRI          nlaIII                 tsp509I    maeIII             csp6I
1801 CTGTGATAAA AATATAGCTT AGTGCTAAAA TCAGTGTAAC TTATACATGG CCTAAAATGT TTCTACAAAT TAGAGTTTGT CACTTATTCC ATTTGTACCT
     GACACTATTT TTATATCGAA TCACGATTTT AGTCACATTG AATATGTACC GGATTTTACA AAGATGTTTA ATCTCAAACA GTGAATAAGG TAAACATGGA
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                                        scrFI[dcm-]
                                        pspGI
                                        mvaI
                                        ecoRII[dcm-]
                                        dsaV[dcm-]
                                        bstNI
                                      haeIII/palI
                                     mscI/ballI[dcm-]
                                     eaeI[dcm-]
                                     cfrI
                                    scrFI[dcm-]
                                    pspGI
                                    mvaI bssKI[dcm-]
                                    ecoRII[dcm-]   tsp45I
                                    dsaV[dcm-]  .  maeIII                                    bssS
                                    bstNI     hinPI                                          hpy18
                                    bssKI[dcm-]  tspRI                                       sau3AI
                               pleI bslI[dcm-] hhaI/cfoI                          styI cac8I  mboI/nd
                  ddeI         mlyI bsaJI apyI[dcm+]                 ddeI          haeIII/palI  dpnII[d
                  bspCNI       hinfI apyI[dcm+]  btsI                bspCNI      mnlI bsaJI     dpnI[da
1901 AAGAGAAAAA TAGGCTCAGT TAGAAAAGGA CTCCCTGGCC AGGCGCAGTG ACTTACGCCT GTAATCTCAG CACTTTGGGA GGCCAAGGCA GGCAGATCAC
     TTCTCTTTTT ATCCGAGTCA ATCTTTTCCT GAGGGACCGG TCCGCGTCAC TGAATGCGGA CATTAGAGTC GTGAAACCCT CCGGTTCCGT CCGTCTAGTG
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                      mscI/balI[dcm-]
                      eaeI[dcm-]
                    scrFI[dcm-]
                    pspGI
                    mvaI
                    ecoRII[dcm-]
                    dsaV[dcm-]
                    bstNI
              bsmAI bssKI[dcm-]
            taqI  fokI cfrI   nlaIII        bsmAI
     hpy188III bsaI bstF5I haeIII/palI      esp3I                 aluI
 mnlI       hpy188III apyI[dcm+]  hphI      bsmBI               tsp509I            nlaIV
2001 GAGGTCAGGA GTTCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT ATAAAAATTA GCTGGGTGTG GTGGCAGGAG CCTGTAATCC
     CTCCAGTCCT CAAGCTCTGG TAGGACCGGT TGTACCACTT TGGGGCAGAG ATGATTTTTA TATTTTTAAT CGACCCACAC CACCGTCCTC GGACATTAGG

                                                                                        scrFI[dcm-]
                                                                                        pspGI
                                                                                        mvaI
                                                                                        ecoRII[dcm-]
                                                                          tspRI         dsaV[dcm-]
                                                                     sau3AI btsI        bstNI
            ddeI       tfiI        hpy188III                         mboI/ndeII[dam-]   bssKI[dcm-]
            bspCNI     hinfI      ddeI                               dpnII[dam-] hpyCH4V apyI[dcm+]
  aluI    mnlI mnlI bssSI         bspCNI      mnlI    tspRI          dpnI[dam+] bsgI  bpmI/gsuI[dcm-]
2101 CAGCTACACA GGAGGCTGAG GCACGAGAAT CACTTGAACT CAGGAGATGG AGGTTTCAGT GAGCCGAGAT CACGCCACTG CACTCCAGCC TGGCAACAGA
     GTCGATGTGT CCTCCGACTC CGTGCTCTTA GTGAACTTGA GTCCTCTACC TCCAAAGTCA CTCGGCTCTA GTGCGGTGAC GTGAGGTCGG ACCGTTGTCT
```

```
                                                        fnu4HI/bsoFI
                                                       haeIII/palI
                                                      mcrI
                                                      eagI/xmaIII/eclXI
                                                      eaeI
                                                      cfrI
          pleI                                        bsiEI      rmaI
          mlyI                                      notI         maeI
          hinfI                                     fnu4HI/bsoFI bfaI
        bsmAI                                       aciI aciI  speI
2201 GCGAGACTCC ATCTCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCCGA CTAGTGAGC
     CGCTCTGAGG TAGAGTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTCCC GCCGGCGGCT GATCACTCG
```

> length: 2269

accI(GTMKAC):	1501
aciI(CCGC):	39 498 2250 2254
aflIII(ACRYGT):	780 1586
ahaIII(TTTAAA):	1150
ahdI(GACNNNNNGTC):	278 714
aluI(AGCT):	152 300 429 510 690 822 888 1015 1345 1476 1816 2070 2102
alw26I(CAGNNNCTG):	101 316
alwI(GGATCNNNN):	318 530
alwNI(CAGNNNCTG):	101 316
apoI(RAATTY):	3 310 423 655 1464
apyI(CCWGG):	321 332 1422 1934 1939 2023 2189
asp700(GAANNNNTTC):	1464 1749
aspHI(GWGCWC):	1582